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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/854,356

DATE: 06/07/2001  
TIME: 17:01:19

Input Set : C:\PAOLA\09854356.txt  
Output Set: C:\CRF3\06072001\I854356.raw

3 <110> APPLICANT: Cheever, Martin A.  
 4       Gheysen, Dirk  
 5       Corixa Corporation  
 6       SmithKline Beecham Biologicals S. A.  
 8 <120> TITLE OF INVENTION: HER-2/neu Fusion Proteins  
 10 <130> FILE REFERENCE: 014058-009810PC  
 12 <140> CURRENT APPLICATION NUMBER: 09/854,356  
 13 <141> CURRENT FILING DATE: 2001-05-09  
 15 <150> PRIOR APPLICATION NUMBER: US 09/493,480  
 16 <151> PRIOR FILING DATE: 2000-01-28  
 18 <150> PRIOR APPLICATION NUMBER: US 60/117,976  
 19 <151> PRIOR FILING DATE: 1999-01-29  
 21 <160> NUMBER OF SEQ ID NOS: 26  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1255  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: human HER-2/neu protein  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: DOMAIN  
 35 <222> LOCATION: (1)..(653)  
 36 <223> OTHER INFORMATION: extracellular domain (ECD)  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: DOMAIN  
 40 <222> LOCATION: (676)..(1255)  
 41 <223> OTHER INFORMATION: intracellular domain (ICD)  
 43 <220> FEATURE:  
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 45 <222> LOCATION: (990)..(1255)  
 46 <223> OTHER INFORMATION: phosphorylation domain (PD)  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: DOMAIN  
 50 <222> LOCATION: (990)..(1048)  
 51 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
 52       portion (delta PD)  
 54 <400> SEQUENCE: 1  
 55 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu  
 56       1                   5                   10                   15  
 58 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys  
 59       20                  25                  30  
 61 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
 62       35                  40                  45  
 64 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
 65       50                  55                  60  
 67 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val

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68	65	70	75	80												
70	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
71				85						90						95
73	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
74					100				105							110
76	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro
77					115			120								125
79	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
80					130			135			140					
82	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
83	145				150					155						160
85	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
86					165			170								175
88	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
89					180			185			190					
91	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser
92					195			200			205					
94	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys
95					210			215			220					
97	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys
98	225				230			235			240					
100	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu
101					245			250			255					
103	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
104					260			265			270					
106	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg
107					275			280			285					
109	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu
110					290			295			300					
112	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
113	305				310				315							320
115	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
116					325			330			335					
118	Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu
119					340			345			350					
121	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys
122					355			360			365					
124	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp
125					370			375			380					
127	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe
128	385				390				395							400
130	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro
131					405			410			415					
133	Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg
134					420			425			430					
136	Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu
137					435			440			445					
139	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly
140					450			455			460					

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**Output Set: C:\CRF3\06072001\I854356.raw**

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142 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
143 465 470 475 480
145 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
146 485 490 495
148 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
149 500 505 510
151 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
152 515 520 525
154 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
155 530 535 540
157 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
158 545 550 555 560
160 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
161 565 570 575
163 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
164 580 585 590
166 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
167 595 600 605
169 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Gly Ala Cys Gln
170 610 615 620
172 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
173 625 630 635 640
175 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
176 645 650 655
178 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
179 660 665 670
181 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
182 675 680 685
184 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
185 690 695 700
187 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
188 705 710 715 720
190 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
191 725 730 . 735
193 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
194 740 745 750
196 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
197 755 760 765
199 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
200 770 775 780
202 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
203 785 790 795 800
205 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
206 805 810 815
208 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
209 820 825 830
211 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
212 835 840 845
214 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe

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215 850 855 860  
217 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp  
218 865 870 875 880  
220 Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg  
221 885 890 895  
223 Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val  
224 900 905 910  
226 Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala  
227 915 920 925  
229 Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro  
230 930 935 940  
232 Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met  
233 945 950 955 960  
235 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe  
236 965 970 975  
238 Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu  
239 980 985 990  
241 Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu  
242 995 1000 1005  
244 Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu  
245 1010 1015 1020  
247 Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly  
248 1025 1030 1035 1040  
250 Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly  
251 1045 1050 1055  
253 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Ala Pro Arg  
254 1060 1065 1070  
256 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly  
257 1075 1080 1085  
259 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His  
260 1090 1095 1100  
262 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu  
263 1105 1110 1115 1120  
265 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln  
266 1125 1130 1135  
268 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro  
269 1140 1145 1150  
271 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu  
272 1155 1160 1165  
274 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val  
275 1170 1175 1180  
277 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln  
278 1185 1190 1195 1200  
280 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala  
281 1205 1210 1215  
283 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala  
284 1220 1225 1230  
286 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr  
287 1235 1240 1245

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Input Set : C:\PAOLA\09854356.txt  
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289 Leu Gly Leu Asp Val Pro Val  
290 1250 1255  
293 <210> SEQ ID NO: 2  
294 <211> LENGTH: 1256  
295 <212> TYPE: PRT  
296 <213> ORGANISM: Rattus sp.  
298 <220> FEATURE:  
299 <223> OTHER INFORMATION: rat HER-2/neu protein  
301 <220> FEATURE:  
302 <221> NAME/KEY: DOMAIN  
303 <222> LOCATION: (1)..(654)  
304 <223> OTHER INFORMATION: extracellular domain (ECD)  
306 <220> FEATURE:  
307 <221> NAME/KEY: DOMAIN  
308 <222> LOCATION: (677)..(1256)  
309 <223> OTHER INFORMATION: intracellular domain (ICD)  
311 <220> FEATURE:  
312 <221> NAME/KEY: DOMAIN  
313 <222> LOCATION: (721)..(998)  
314 <223> OTHER INFORMATION: kinase domain (KD)  
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317 <221> NAME/KEY: DOMAIN  
318 <222> LOCATION: (991)..(1256)  
319 <223> OTHER INFORMATION: phosphorylation domain (PD)  
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322 <221> NAME/KEY: DOMAIN  
323 <222> LOCATION: (991)..(1049)  
324 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
325 portion (delta PD)  
327 <400> SEQUENCE: 2  
328 Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu  
329 1 5 10 15  
331 Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys  
332 20 25 30  
334 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
335 35 40 45  
337 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
338 50 55 60  
340 Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
341 65 70 75 80  
343 Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu  
344 85 90 95  
346 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr  
347 100 105 110  
349 Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala  
350 115 120 125  
352 Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg  
353 130 135 140  
355 Ser Leu Thr Glu Ile Leu Lys Gly Val Leu Ile Arg Gly Asn Pro

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/09/854,356

DATE: 06/07/2001  
TIME: 17:01:21

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